



54600-8130.US00-SEQLIST.TXT

SEQUENCE LISTING

<110> Lim, Moon Young
Edwards, Cynthia A.
Fry, Kirk E.
Bruice, Thomas W.
Starr, Douglas B.
Laurance, Megan E.
Kwok, Yan

<120> DNA Binding Compound-Mediated Molecular
Switch System

<130> 4600-0130.30

<140> US 09/518,297
<141> 2000-03-03

<150> US 60/122,513
<151> 1999-03-03

<150> US 60/154,605
<151> 1999-09-17

<160> 77

<170> FastSEQ for Windows Version 4.0

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<220>
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<400> 1
cgttcgact t

11

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<220>
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<400> 2
cggagtactg tcctccg

17

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<220>
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<221> misc_feature
<222> (1)...(12)
<223> n = A,T,C or G

<400> 3
taattanggg ng

12

<210> 4
<211> 551
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (0)...(0)
<223> transcriptional regulatory protein

<400> 4
Met Asp Glu Leu Phe Pro Leu Ile Phe Pro Ala Glu Pro Ala Gln Ala
1 5 10 15
Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met
20 25 30
Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly
35 40 45
Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn
50 55 60
Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp
65 70 75 80
Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg
85 90 95
Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser
100 105 110
Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln
115 120 125
Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro
130 135 140
Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys
145 150 155 160
Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro
165 170 175
Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala
180 185 190
Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly
195 200 205
Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu Asp Ile
210 215 220
Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser
225 230 235 240
Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro
245 250 255
Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val Arg Val Ser Met Gln Leu
260 265 270
Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu Pro Met Glu Phe Gln Tyr
275 280 285
Leu Pro Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg
290 295 300
Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys Ser Pro Phe Ser Gly
305 310 315 320
Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg Ile Ala Val Pro Ser Arg
325 330 335
Ser Ser Ala Ser Val Pro Lys Pro Ala Pro Gln Pro Tyr Pro Phe Thr
340 345 350
Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu Phe Pro Thr Met Val Phe
355 360 365
Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala Leu Ala Pro Ala Pro Pro
370 375 380

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Gln Val Leu Pro Gln Ala Pro Ala Pro Ala Pro Ala Met Val
 385 390 395 400
 Ser Ala Leu Ala Gln Ala Pro Ala Pro Val Pro Val Leu Ala Pro Gly
 405 410 415
 Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys Pro Thr Gln Ala Gly
 420 425 430
 Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp Glu
 435 440 445
 Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp Pro Ala Val Phe Thr
 450 455 460
 Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln
 465 470 475 480
 Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro Met Leu Met Glu Tyr
 485 490 495
 Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala Gln Arg Pro Pro Asp
 500 505 510
 Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu
 515 520 525
 Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala
 530 535 540
 Leu Leu Ser Gln Ile Ser Ser
 545 550

<210> 5
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<220>
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<400> 5
 tccctatcag tgatagaga

19

<210> 6
 <211> 22
 <212> DNA
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<220>
 <223> response element

<400> 6
 cttaacactc gcgagtgtta ag

22

<210> 7
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 <223> n = A,T,C or G

<221> misc_feature
 <222> (12)...(12)

<223> n = A or C

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rgntcantga cny

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<211> 77
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Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp Leu
20 25 30
Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro His
35 40 45
Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe Glu
50 55 60
Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly
65 70 75<210> 9
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<223> activator sequence<221> VARIANT
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<223> tetramer<400> 9
Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
1 5 10<210> 10
<211> 97
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<213> Artificial Sequence<220>
<223> repressor sequence<400> 10
Met Asp Ala Lys Ser Leu Thr Ala Trp Ser Arg Thr Leu Val Thr Phe
1 5 10 15
Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys Leu Leu Asp
20 25 30
Thr Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu Asn Tyr Lys
35 40 45
Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp Val Ile Leu
50 55 60
Arg Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg Glu Ile His
65 70 75 80
Gln Glu Thr His Pro Asp Ser Glu Thr Ala Phe Glu Ile Lys Ser Ser
85 90 95
Val

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<210> 11
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> repressor sequence

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Met Ala Ala Ala Val Arg Met Asn Ile Gln Met Leu Leu Glu Ala Ala
1 5 10 15
Asp Tyr Leu Glu Arg Arg Glu Arg Glu Ala Glu His Gly Tyr Ala Ser
20 25 30
Met Leu Pro Tyr
35

<210> 12
<211> 116
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (0)...(0)
<223> partial promoter sequence

<400> 12
cgcggtcaga aaatttatttt aaatttcctc ttgtcaggcc ggaataactc cctataatgc 60
gccaccactg acacggaaca acggcaaaca cgccgccggg tcagcgggt tctcct 116

<210> 13
<211> 22
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (0)...(0)
<223> partial promoter sequence

<400> 13
agaaaattat tttaaatttc ct 22

<210> 14
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> modified promoter sequence

<400> 14
gactgcagtg gtaccttagga gg 22

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> modified promoter sequence

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<400> 15		
agaaaattat ttaaatttc ct	22	
<210> 16		
<211> 22		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> modified promoter sequence		
<400> 16		
ggaaaatttt ttttcaaaag ta	22	
<210> 17		
<211> 22		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> modified promoter sequence		
<400> 17		
tgaaatttat tttgcgaaag gg	22	
<210> 18		
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<212> DNA		
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<220>		
<223> engineered DNA response element		
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tgttcgact t	11	
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catggacgcc actgagccgt ttttggcg acttgaggcg agtcgatgca cc	52	
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catggacgcc actgagccgt gttcgactt tttttgagg cgagtcgatg cacc	54	
<210> 21		
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<220>
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<400> 21
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<220>
<223> engineered DNA response element

<400> 22
cttaaaaata ac 12

<210> 23
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 23
ttgaaaaatc aacgct 16

<210> 24
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 24
tttttggcg cactttttt t 21

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 25
tttttgggat tttccttttt 20

<210> 26
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 26
aaaaaaattgt gagcgctcac aatttttt 28

<210> 27

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<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> tissue-specific transcription factor

<400> 27
acttta 6

<210> 28
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 28
taccgacat 9

<210> 29
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 29
gggactttcc 10

<210> 30
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 30
gggattttcc 10

<210> 31
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 31
cgaccgtgct cgagttaacg ggactttcca aaaacgatcg gactggactc 50

<210> 32
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 32

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cgaccgtgct cgagttAACG ggatTTCCA aaaACGATCG gACTGGACTC	50
<210> 33	
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<223> engineered DNA response element	
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cgaccgtgct cgagAAATTG ggatTTCCA aaaACGATCG gACTGGACTC	50
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<211> 28	
<212> DNA	
<213> Artificial Sequence	
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<223> engineered DNA response element	
<400> 34	
aaaaAAATTGT gagCGCTCAC AATTTTT	28
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<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> engineered DNA response element	
<400> 35	
TTTTTTTGT gagCGGATAA CAAAA	25
<210> 36	
<211> 10	
<212> DNA	
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<220>	
<223> engineered DNA response element	
<400> 36	
tCTGGGATCC	10
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<211> 14	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> engineered DNA response element	
<400> 37	
gAGTTTTTT TAAG	14
<210> 38	
<211> 14	
<212> DNA	
<213> Artificial Sequence	
<220>	

<223> engineered DNA response element

<400> 38

gagttttaaa agag

14

<210> 39

<211> 969

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (0)...(0)

<223> transcriptional regulatory protein

<400> 39

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 1 5 10 15
 Leu Asp Pro Ser Leu Thr His Thr Ile Phe Asn Pro Glu Val Phe Gln
 20 25 30
 Pro Gln Met Ala Leu Pro Thr Ala Asp Gly Pro Tyr Leu Gln Ile Leu
 35 40 45
 Glu Gln Pro Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys Glu Gly
 50 55 60
 Pro Ser His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn Lys Lys
 65 70 75 80
 Ser Tyr Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala Lys Val
 85 90 95
 Ile Val Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His Ala His
 100 105 110
 Ser Leu Val Gly Lys His Cys Glu Asp Gly Ile Cys Thr Val Thr Ala
 115 120 125
 Gly Pro Lys Asp Met Val Val Gly Phe Ala Asn Leu Gly Ile Leu His
 130 135 140
 Val Thr Lys Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met Thr Glu
 145 150 155 160
 Ala Cys Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Pro Asp Leu
 165 170 175
 Ala Tyr Leu Gln Ala Glu Gly Gly Asp Arg Gln Leu Gly Asp Arg
 180 185 190
 Glu Lys Glu Leu Ile Arg Gln Ala Ala Leu Gln Gln Thr Lys Glu Met
 195 200 205
 Asp Leu Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro Asp Ser
 210 215 220
 Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp Ala Ile
 225 230 235 240
 Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val Arg Met
 245 250 255
 Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr Leu Leu
 260 265 270
 Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr Glu Glu
 275 280 285
 Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser Pro Thr
 290 295 300
 Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys Tyr Lys
 305 310 315 320
 Asp Ile Asn Ile Thr Lys Pro Ala Ser Val Phe Val Gln Leu Arg Arg
 325 330 335
 Lys Ser Asp Leu Glu Thr Ser Glu Pro Lys Pro Phe Leu Tyr Tyr Pro
 340 345 350
 Glu Ile Lys Asp Lys Glu Glu Val Gln Arg Lys Arg Gln Lys Leu Met
 355 360 365
 Pro Asn Phe Ser Asp Ser Phe Gly Gly Ser Gly Ala Gly Ala Gly

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370 Gly Gly Gly Met Phe Gly Ser Gly Gly Gly Gly Gly Thr Gly Ser
 385 375 390 395 395 400
 Thr Gly Pro Gly Tyr Ser Phe Pro His Tyr Gly Phe Pro Thr Tyr Gly
 405 410 415
 Gly Ile Thr Phe His Pro Gly Thr Thr Lys Ser Asn Ala Gly Met Lys
 420 425 430
 His Gly Thr Met Asp Thr Glu Ser Lys Lys Asp Pro Glu Gly Cys Asp
 435 440 445
 Lys Ser Asp Asp Lys Asn Thr Val Asn Leu Phe Gly Lys Val Ile Glu
 450 455 460
 Thr Thr Glu Gln Asp Gln Glu Pro Ser Glu Ala Thr Val Gly Asn Gly
 465 470 475 480
 Glu Val Thr Leu Thr Tyr Ala Thr Gly Thr Lys Glu Glu Ser Ala Gly
 485 490 495
 Val Gln Asp Asn Leu Phe Leu Glu Lys Ala Met Gln Leu Ala Lys Arg
 500 505 510
 His Ala Asn Ala Leu Phe Asp Tyr Ala Val Thr Gly Asp Val Lys Met
 515 520 525
 Leu Leu Ala Val Gln Arg His Leu Thr Ala Val Gln Asp Glu Asn Gly
 530 535 540
 Asp Ser Val Leu His Leu Ala Ile Ile His Leu His Ser Gln Leu Val
 545 550 555 560
 Arg Asp Leu Leu Glu Val Thr Ser Gly Leu Ile Ser Asp Asp Ile Ile
 565 570 575
 Asn Met Arg Asn Asp Leu Tyr Gln Thr Pro Leu His Leu Ala Val Ile
 580 585 590
 Thr Lys Gln Glu Asp Val Val Glu Asp Leu Leu Arg Ala Gly Ala Asp
 595 600 605
 Leu Ser Leu Leu Asp Arg Leu Gly Asn Ser Val Leu His Leu Ala Ala
 610 615 620
 Lys Glu Gly His Asp Lys Val Leu Ser Ile Leu Leu Lys His Lys Lys
 625 630 635 640
 Ala Ala Leu Leu Leu Asp His Pro Asn Gly Asp Gly Leu Asn Ala Ile
 645 650 655
 His Leu Ala Met Met Ser Asn Ser Leu Pro Cys Leu Leu Leu Val
 660 665 670
 Ala Ala Gly Ala Asp Val Asn Ala Gln Glu Gln Lys Ser Gly Arg Thr
 675 680 685
 Ala Leu His Leu Ala Val Glu His Asp Asn Ile Ser Leu Ala Gly Cys
 690 695 700
 Leu Leu Leu Glu Gly Asp Ala His Val Asp Ser Thr Thr Tyr Asp Gly
 705 710 715 720
 Thr Thr Pro Leu His Ile Ala Ala Gly Arg Gly Ser Thr Arg Leu Ala
 725 730 735
 Ala Leu Leu Lys Ala Ala Gly Ala Asp Pro Leu Val Glu Asn Phe Glu
 740 745 750
 Pro Leu Tyr Asp Leu Asp Asp Ser Trp Glu Asn Ala Gly Glu Asp Glu
 755 760 765
 Gly Val Val Pro Gly Thr Thr Pro Leu Asp Met Ala Thr Ser Trp Gln
 770 775 780
 Val Phe Asp Ile Leu Asn Gly Lys Pro Tyr Glu Pro Glu Phe Thr Ser
 785 790 795 800
 Asp Asp Leu Leu Ala Gln Gly Asp Met Lys Gln Leu Ala Glu Asp Val
 805 810 815
 Lys Leu Gln Leu Tyr Lys Leu Leu Glu Ile Pro Asp Pro Asp Lys Asn
 820 825 830
 Trp Ala Thr Leu Ala Gln Lys Leu Gly Leu Gly Ile Leu Asn Asn Ala
 835 840 845
 Phe Arg Leu Ser Pro Ala Pro Ser Lys Thr Leu Met Asp Asn Tyr Glu
 850 855 860
 Val Ser Gly Gly Thr Val Arg Glu Leu Val Glu Ala Leu Arg Gln Met
 865 870 875 880

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Gly Tyr Thr Glu Ala Ile Glu Val Ile Gln Ala Ala Ser Ser Pro Val
 885 890 895
 Lys Thr Thr Ser Gln Ala His Ser Leu Pro Leu Ser Pro Ala Ser Thr
 900 905 910
 Arg Gln Gln Ile Asp Glu Leu Arg Asp Ser Asp Ser Val Cys Asp Thr
 915 920 925
 Gly Val Glu Thr Ser Phe Arg Lys Leu Ser Phe Thr Glu Ser Leu Thr
 930 935 940
 Ser Gly Ala Ser Leu Leu Thr Leu Asn Lys Met Pro His Asp Tyr Gly
 945 950 955 960
 Gln Glu Gly Pro Leu Glu Gly Lys Ile
 965

<210> 40
 <211> 96
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> engineered regulatory sequence

<400> 40
 gctagccccg ccccggttgac gcaaatgggc ggttaggcgtg tacgggtggga ggtttatata 60
 agcagagctc gtttagtgaa ccgtcagatc agatct 96

<210> 41
 <211> 154
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> engineered regulatory sequence

<400> 41
 gctagcgccc aaattgggat tttccaaaaaa gccgaaattg ggattttcca aaaaccgccc 60
 atcggccggcc ccgttgacgc aaatgggcgg taggcgtgtt cgggtggagg tttatataag 120
 cagagctcgt ttagtgaacc gtcagatc atct 154

<210> 42
 <211> 212
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> engineered regulatory sequence

<400> 42
 acgcgtgccc aaattgggat tttccaaaaaa gccgaaattg ggattttcca aaaaccgcgc 60
 tagcgcccaa attgggattt tccaaaaagc cggaaattggg atttccaaa aaccgcccgt 120
 cggccggccc gttgacgcgtt atggcggtt ggcgtgtacg gtgggagggtt tatataagca 180
 gagctcggtt agtgaaccgt cagatcagat ct 212

<210> 43
 <211> 96
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> engineered regulatory sequence

<400> 43
 gctagccccg ccccggttgac gcaaatgggc ggttaggcgtg tacgggtggga ggtcttatata 60
 agcagagctc gtttagtgaa ccgtcagatc agatct 96

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<210> 44
<211> 154
<212> DNA
<213> Artificial Sequence

<220>
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<400> 44
gctagcggcc aggtcggat tttccgagga gccgaggctcg ggattttccg aggaccgccc 60
atcgccgcgc ccgttgacgc aaatgggcgg taggcgtgta cggtgggagg cctatataag 120
cagagctcgt ttagtgaacc gtcagatcag atct 154

<210> 45
<211> 154
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered regulatory sequence

<400> 45
gctagcggcc aggtcggat tttccgagga gccgaggctcg ggattttccg aggaccgccc 60
atcgccgcgc ccgttgacgc aaatgggcgg taggcgtgta cggtgggagg cctatataag 120
cagagctcgt ttagtgaacc gtcagatcag atct 154

<210> 46
<211> 762
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered promoter construct

<400> 46
ggtaacctaa tattggccat tagccatatt attcattggt tatatacgat aaattaat 60
tggctattgg ccattgcata cgttgatct atatcataat atgtacattt atattggctc 120
atgtccaata tgaccgccc gttggcattt attattgact agttattaat agtaatcaat 180
tacggggtca ttagttcata gcccataat ggagttccgc gttacataac ttacggtaaa 240
tggccgcct ggctgaccgc ccaacgaccc cggcccatgg acgtcaataa tgacgtatgt 300
tccccatagta acgcaaataag ggattttcca ttaacgtcaa tgggtggagt atttacggta 360
aactgcccac ttggcagtac atcaagtgtt tcataatgcca agtccgcccc ctattgacgt 420
caatgacggt aaatggcccg cctggcatta tgcccagttac atgactttat gggattttcc 480
tatttggcag tacatctacg tattagtcat cgctattacc atgggtatgc ggttttggca 540
gtacaccaat gggcgtggat agcgggttga ctcacgggaa tttccaagtc tccaccccat 600
tgacgtcaat gggagtttg tttggcacca aggtaaaagg gattttccaa aatgtcgtaa 660
caactgcat cggccgcggcc gttgacgcaa atgggcggta ggcgtgtacg gtgggaggtt 720
tatataagca gagctcgaaa agtgaaccgt cagatcaagc tt 762

<210> 47
<211> 762
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered promoter construct

<400> 47
ggtaacctaa tattggccat tagccatatt attcattggt tatatacgat aaattaat 60
tggctattgg ccattgcata cgttgatct atatcataat atgtacattt atattggctc 120
atgtccaata tgaccgccc gttggcattt attattgact agttattaat agtaatcaat 180
tacggggtca ttagttcata gcccataat ggagttccgc gttacataac ttacggtaaa 240

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tggccgcct	ggctgaccgc	ccaaacgaccc	ccgcccattt	acgtcaataa	tgacgtatgt	300
tcccata	acgcaaataat	tcccgaaa	ttaacgtcaa	tgggtggagt	atttacggta	360
aactgcccac	ttggcagtac	atcaagtgt	tcatatgcca	agtccgcccc	ctattgacgt	420
caatgacgg	aatatggcccg	cctggcatta	tgcccagttac	atgactttat	tctcgaggaa	480
tatttggcag	tacatctacg	tattagtcat	cgctattacc	atgggtatgc	ggttttggca	540
gtacaccaat	gggcgtggat	agcggttga	ctcacgggga	tttccaagtc	tccacccat	600
tgacgtcaat	gggagttgt	tttggcacca	aggtaaaatt	acgcgtaaaaa	aatgtcgtaa	660
caactgcgt	cggccgcccc	gttgcaccaa	atgggcggta	ggcgtgtacg	gtgggagggtt	720
gctagccgca	gagctcg	ttt	agtgaaccgt	cagatcaagc	tt	762

<210> 48

<211> 762

<212> DNA

<213> Artificial Sequence

<220>

<223> engineered promoter construct

<400> 48

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atgtccaata	tgaccgcatt	gttggcattt	attattgact	agttattaaat	agtaatcaat	180
tacggggtca	ttagttcata	gcccataat	ggagttccgc	gttacataac	ttacggtaaa	240
tggccgcct	ggctgaccgc	ccaaacgaccc	ccgcccattt	acgtcaataa	tgacgtatgt	300
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